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Substitute Sequence Listing

<110> SCHUIJFFEL, Danielle Francisca
 NUIJTEN, Petrus Johannes Maria

<120> Ornithobacterium rhinotracheale subunit vaccines

<130> I-2004.011 US

<140>
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<150> PCT/EP2005/050577
 <151> 2005-02-09

<150> EP 04075427.7
 <151> 2004-02-11

<160> 16

<170> PatentIn version 3.3

<210> 1
 <211> 1614
 <212> DNA
 <213> Ornithobacterium rhinotracheale

<220>
 <221> CDS
 <222> (1)..(1614)

<400> 1

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ggg aaa gtg gaa tct tgg aac aaa aaa gta gga gat aaa gta tca tac	96
Gly Lys Val Glu Ser Trp Asn Lys Lys Val Gly Asp Lys Val Ser Tyr	
20 25 30	
ggc gac atc tta gcc gaa atc gaa aca gat aaa gcg gtt caa gaa ttt	144
Gly Asp Ile Leu Ala Glu Ile Glu Thr Asp Lys Ala Val Gln Glu Phe	
35 40 45	
gaa aca gat gta gaa ggt act ctt tta tac atc ggt gta gag gct ggt	192
Glu Thr Asp Val Glu Gly Thr Leu Leu Tyr Ile Gly Val Glu Ala Gly	
50 55 60	
caa gca gca cca gtt gat agt att tta gct atc atc ggt gca gaa ggc	240
Gln Ala Ala Pro Val Asp Ser Ile Leu Ala Ile Ile Gly Ala Glu Gly	
65 70 75 80	
gaa gac atc agc ggt ttg gta agc ggt gga ggt gct agc caa tca gcg	288
Glu Asp Ile Ser Gly Leu Val Ser Gly Gly Gly Ala Ser Gln Ser Ala	
85 90 95	
cca gct caa gaa gct gcc gct cct gca gaa gaa cca caa gcg gaa gct	336
Pro Ala Gln Glu Ala Ala Ala Pro Ala Glu Glu Pro Gln Ala Glu Ala	
100 105 110	
gca cca gcg gct gaa gtt cca gaa aat gta act atc gtt tct atg cca	384
Ala Pro Ala Ala Glu Val Pro Glu Asn Val Thr Ile Val Ser Met Pro	

Substitute Sequence Listing

115	120	125	
aga ttg agc gat acc atg gaa gaa ggt aaa gta gaa tct tgg aac aaa Arg Leu Ser Asp Thr Met Glu Glu Gly Lys Val Glu Ser Trp Asn Lys 130 135 140			432
aaa gta gga gat aaa gta tca tac ggc gac atc tta gcc gaa atc gaa Lys Val Gly Asp Lys Val Ser Tyr Gly Asp Ile Leu Ala Glu Ile Glu 145 150 155 160			480
aca gat aaa gcg gtt caa gaa ttt gaa aca gat gta gaa ggt act tta Thr Asp Lys Ala Val Gln Glu Phe Glu Thr Asp Val Glu Gly Thr Leu 165 170 175			528
tta tat ata ggt gta gaa gct ggg caa tca gca cca gtt gat agc att Leu Tyr Ile Gly Val Glu Ala Gly Gln Ser Ala Pro Val Asp Ser Ile 180 185 190			576
ttg gca atc atc gga cct gaa gga aca gat gtt tct gca atc gta gca Leu Ala Ile Ile Gly Pro Glu Gly Thr Asp Val Ser Ala Ile Val Ala 195 200 205			624
gga ggt ggt gca aaa cca gct gct aaa gcg gaa gct cca aag gct gaa Gly Gly Gly Ala Lys Pro Ala Ala Lys Ala Glu Ala Pro Lys Ala Glu 210 215 220			672
gca cct aag caa gct gct cca gca caa gag aaa aaa gaa act cca gcg Ala Pro Lys Gln Ala Ala Pro Ala Gln Glu Lys Lys Glu Thr Pro Ala 225 230 235 240			720
cct gct gct cca aaa gca caa gct acc aac aat tca ggt aga gta ttt Pro Ala Ala Pro Lys Ala Gln Ala Thr Asn Asn Ser Gly Arg Val Phe 245 250 255			768
att tct cca ttg gct aaa aaa ttg gct gat gaa aaa gga tac gat atc Ile Ser Pro Leu Ala Lys Lys Leu Ala Asp Glu Lys Gly Tyr Asp Ile 260 265 270			816
aat caa att caa ggt aca gga gac aac gga aga atc atc aaa aaa gat Asn Gln Ile Gln Gly Thr Gly Asp Asn Gly Arg Ile Ile Lys Lys Asp 275 280 285			864
gtt gaa aac ttt act cca caa gct gct gcg gct aag cca gct gtt gct Val Glu Asn Phe Thr Pro Gln Ala Ala Ala Lys Pro Ala Val Ala 290 295 300			912
ggt cca gtt gca ttg gaa gta gga gaa gat act gta atc cct aac tct Gly Pro Val Ala Leu Glu Val Gly Glu Asp Thr Val Ile Pro Asn Ser 305 310 315 320			960
caa atg aga aaa gtg att gct aag cgt ctt tct gaa agt aaa ttt aca Gln Met Arg Lys Val Ile Ala Lys Arg Leu Ser Glu Ser Lys Phe Thr 325 330 335			1008
gca cca cac tac tac tta acc att gaa gta gat atg gat aat gtg atg Ala Pro His Tyr Tyr Leu Thr Ile Glu Val Asp Met Asp Asn Val Met 340 345 350			1056
gcg gct cgt aag caa atc aac caa att cca aat aca aaa gta tct ttc Ala Ala Arg Lys Gln Ile Asn Gln Ile Pro Asn Thr Lys Val Ser Phe 355 360 365			1104
aac gat atc gta ttg aag gct act gct atg gct gtg aaa aaa cac cca 1152			

Substitute Sequence Listing																
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Val	Val	Asn	Ser	Thr	Trp 390	Lys	Asp	Asn	Glu	Ile 395	Val	Gln	Tyr	Ala	Ala 400	
gta	aac	atc	ggg	gtt	gca	gtt	gct	gtt	cca	gat	ggg	ctt	gta	gta	cct	1248
Val	Asn	Ile	Gly	Val 405	Ala	Val	Ala	Val	Pro 410	Asp	Gly	Leu	Val	Val 415	Pro	
gta	gtg	aaa	aac	aca	gat	tta	aaa	tca	tta	tct	caa	att	tct	gct	gag	1296
Val	Val	Lys	Asn 420	Thr	Asp	Leu	Lys	Ser 425	Leu	Ser	Gln	Ile	Ser 430	Ala	Glu	
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Val	Lys	Asp 435	Leu	Ala	Thr	Arg	Ser 440	Arg	Asp	Arg	Lys	Ile 445	Lys	Ala	Asp	
gag	atg	gaa	ggg	tct	acc	ttt	aca	gtt	tct	aac	cta	gga	gct	tac	ggg	1392
Glu	Met	Glu	Gly	Ser	Thr	Phe 455	Thr	Val	Ser	Asn	Leu 460	Gly	Ala	Tyr	Gly	
gta	gaa	agc	ttt	aca	tca	atc	atc	aac	cag	cca	aac	tct	tgt	atc	ctt	1440
Val	Glu	Ser	Phe	Thr	Ser 470	Ile	Ile	Asn	Gln	Pro 475	Asn	Ser	Cys	Ile	Leu 480	
tct	gta	ggg	gca	att	gta	gaa	aaa	cca	gtt	gtt	aaa	aac	gga	caa	atc	1488
Ser	Val	Gly	Ala	Ile 485	Val	Glu	Lys	Pro	Val 490	Val	Lys	Asn	Gly	Gln 495	Ile	
gta	gtt	ggg	cac	aca	atg	aaa	ctt	tgt	tta	gct	tgc	gat	cac	aga	act	1536
Val	Val	Gly	His 500	Thr	Met	Lys	Leu	Cys 505	Leu	Ala	Cys	Asp	His 510	Arg	Thr	
gtg	gac	gga	gca	act	gga	agt	act	ttc	cta	caa	act	tta	aaa	caa	tac	1584
Val	Asp	Gly 515	Ala	Thr	Gly	Ser	Thr 520	Phe	Leu	Gln	Thr	Leu 525	Lys	Gln	Tyr	
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<210> 2
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 <212> PRT
 <213> Ornithobacterium rhinotracheale

<400> 2

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Gly Lys Val Glu Ser Trp Asn Lys Lys Val Gly Asp Lys Val Ser Tyr
20 25 30

Gly Asp Ile Leu Ala Glu Ile Glu Thr Asp Lys Ala Val Gln Glu Phe
35 40 45

Substitute Sequence Listing

Glu Thr Asp Val Glu Gly Thr Leu Leu Tyr Ile Gly Val Glu Ala Gly
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 65 70 75 80
 Glu Asp Ile Ser Gly Leu Val Ser Gly Gly Gly Ala Ser Gln Ser Ala
 85 90 95
 Pro Ala Gln Glu Ala Ala Ala Pro Ala Glu Glu Pro Gln Ala Glu Ala
 100 105 110
 Ala Pro Ala Ala Glu Val Pro Glu Asn Val Thr Ile Val Ser Met Pro
 115 120 125
 Arg Leu Ser Asp Thr Met Glu Glu Gly Lys Val Glu Ser Trp Asn Lys
 130 135 140
 Lys Val Gly Asp Lys Val Ser Tyr Gly Asp Ile Leu Ala Glu Ile Glu
 145 150 155 160
 Thr Asp Lys Ala Val Gln Glu Phe Glu Thr Asp Val Glu Gly Thr Leu
 165 170 175
 Leu Tyr Ile Gly Val Glu Ala Gly Gln Ser Ala Pro Val Asp Ser Ile
 180 185 190
 Leu Ala Ile Ile Gly Pro Glu Gly Thr Asp Val Ser Ala Ile Val Ala
 195 200 205
 Gly Gly Gly Ala Lys Pro Ala Ala Lys Ala Glu Ala Pro Lys Ala Glu
 210 215 220
 Ala Pro Lys Gln Ala Ala Pro Ala Gln Glu Lys Lys Glu Thr Pro Ala
 225 230 235 240
 Pro Ala Ala Pro Lys Ala Gln Ala Thr Asn Asn Ser Gly Arg Val Phe
 245 250 255
 Ile Ser Pro Leu Ala Lys Lys Leu Ala Asp Glu Lys Gly Tyr Asp Ile
 260 265 270
 Asn Gln Ile Gln Gly Thr Gly Asp Asn Gly Arg Ile Ile Lys Lys Asp
 275 280 285
 Val Glu Asn Phe Thr Pro Gln Ala Ala Ala Ala Lys Pro Ala Val Ala
 290 295 300

Substitute Sequence Listing

Gly Pro Val Ala Leu Glu Val Gly Glu Asp Thr Val Ile Pro Asn Ser
305 310 315 320

Gln Met Arg Lys Val Ile Ala Lys Arg Leu Ser Glu Ser Lys Phe Thr
325 330 335

Ala Pro His Tyr Tyr Leu Thr Ile Glu Val Asp Met Asp Asn Val Met
340 345 350

Ala Ala Arg Lys Gln Ile Asn Gln Ile Pro Asn Thr Lys Val Ser Phe
355 360 365

Asn Asp Ile Val Leu Lys Ala Thr Ala Met Ala Val Lys Lys His Pro
370 375 380

Val Val Asn Ser Thr Trp Lys Asp Asn Glu Ile Val Gln Tyr Ala Ala
385 390 395 400

Val Asn Ile Gly Val Ala Val Ala Val Pro Asp Gly Leu Val Val Pro
405 410 415

Val Val Lys Asn Thr Asp Leu Lys Ser Leu Ser Gln Ile Ser Ala Glu
420 425 430

Val Lys Asp Leu Ala Thr Arg Ser Arg Asp Arg Lys Ile Lys Ala Asp
435 440 445

Glu Met Glu Gly Ser Thr Phe Thr Val Ser Asn Leu Gly Ala Tyr Gly
450 455 460

Val Glu Ser Phe Thr Ser Ile Ile Asn Gln Pro Asn Ser Cys Ile Leu
465 470 475 480

Ser Val Gly Ala Ile Val Glu Lys Pro Val Val Lys Asn Gly Gln Ile
485 490 495

Val Val Gly His Thr Met Lys Leu Cys Leu Ala Cys Asp His Arg Thr
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Leu Glu Thr Pro Met Ser Met Leu Val
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<210> 3
<211> 1572

Substitute Sequence Listing

<212> DNA

<213> Ornithobacterium rhinotracheale

<220>

<221> CDS

<222> (1)..(1572)

<400> 3

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ttt gca gca tgt agc gat ttt gat tac aat gta gaa aac cca aac ctc	96
Phe Ala Ala Cys Ser Asp Phe Asp Tyr Asn Val Glu Asn Pro Asn Leu	
20 25 30	
acg aag gga gag gct gat ttc tct aaa tat gta gct tta gga aat tct	144
Thr Lys Gly Glu Ala Asp Phe Ser Lys Tyr Val Ala Leu Gly Asn Ser	
35 40 45	
ctc act tct ggt tat tca gac gga gcc tta tat cgc tcg gca caa gag	192
Leu Thr Ser Gly Tyr Ser Asp Gly Ala Leu Tyr Arg Ser Ala Gln Glu	
50 55 60	
aat tca tac ccc gca atc att gcc aaa caa atg aaa tat gta ggc ggt	240
Asn Ser Tyr Pro Ala Ile Ile Ala Lys Gln Met Lys Tyr Val Gly Gly	
65 70 75 80	
ggc gag ttc tct caa cct ttg atg aaa gac aac att ggt ggt ttt tcg	288
Gly Glu Phe Ser Gln Pro Leu Met Lys Asp Asn Ile Gly Gly Phe Ser	
85 90 95	
gat ttg ttt gaa gca agt aaa cac acc gca ttt tac gga aaa tta gaa	336
Asp Leu Phe Glu Ala Ser Lys His Thr Ala Phe Tyr Gly Lys Leu Glu	
100 105 110	
tta aaa atc gta gac ggt gca cct acg cca gtg cct tct gtg cct aag	384
Leu Lys Ile Val Asp Gly Ala Pro Thr Pro Val Pro Ser Val Pro Lys	
115 120 125	
ttt agt tta gct caa acc ttc gta aaa ggg aat ttt aat aat ttg ggc	432
Phe Ser Leu Ala Gln Thr Phe Val Lys Gly Asn Phe Asn Asn Leu Gly	
130 135 140	
gtg cca ggg gct aaa tct tat cat tta tta gct caa ggt tac gga aat	480
Val Pro Gly Ala Lys Ser Tyr His Leu Leu Ala Gln Gly Tyr Gly Asn	
145 150 155 160	
att gct aat ctg aag gag agt aaa gcc aat cca tat ttt gtg cga ttt	528
Ile Ala Asn Leu Lys Glu Ser Lys Ala Asn Pro Tyr Phe Val Arg Phe	
165 170 175	
gct agc caa cca aat gcc agc gtg ctg agc gat gct ttg gca caa aaa	576
Ala Ser Gln Pro Asn Ala Ser Val Leu Ser Asp Ala Leu Ala Gln Lys	
180 185 190	
cct aca ttc ttt acc tta tgg atc ggg aac aac gat gtt tta ggc tat	624
Pro Thr Phe Phe Thr Leu Trp Ile Gly Asn Asn Asp Val Leu Gly Tyr	
195 200 205	
gcc atg aat ggc gca gca agc aca gat cga aaa ggg aac cct gat gta	672
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Substitute Sequence Listing

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ttg Leu 245	gtg Val 245	gca Ala 250	ggc Gly 250
720			
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tta Leu 260	gta Val 260	aaa Lys 265	gca Ala 270
768			
gct Ala 270	gta Val 270	gca Ala 275	aat Asn 280
ttg Leu 280	cct Pro 280	tat Tyr 285	gtc Val 290
816			
gaa Glu 290	gac Asp 295	att Ile 300	ccg Pro 305
tat Tyr 310	ttt Phe 315	aca Thr 320	acc Thr 325
864			
gtg Val 330	ccg Pro 335	gct Ala 340	gag Glu 345
cct Pro 350	tta Leu 355	agc Ser 360	ttt Phe 365
912			
att Ile 370	gaa Glu 375	aat Asn 380	aaa Lys 385
ttg Leu 390	aat Asn 395	aaa Lys 400	ttt Phe 405
960			
gcc Ala 410	cta Leu 415	gga Gly 420	gca Ala 425
agc Ser 430	ggt Gly 435	gct Ala 440	gtg Val 445
1008			
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ttt Phe 470	ttt Phe 475	gta Val 480	gct Ala 485
1056			
atc Ile 490	tta Leu 495	gca Ala 500	acc Thr 505
ttt Phe 510	ggt Gly 515	caa Gln 520	gtg Val 525
1104			
cta Leu 530	aaa Lys 535	gta Val 540	gca Ala 545
ttt Phe 550	ggt Gly 555	caa Gln 560	gtg Val 565
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ttt Phe 630	ggt Gly 635	caa Gln 640	gtg Val 645
1248			
gaa Glu 650	gta Val 655	gca Ala 660	ggt Gly 665
ttt Phe 670	ggt Gly 675	caa Gln 680	gtg Val 685
1296			
gaa Glu 690	gta Val 695	gca Ala 700	ggt Gly 705
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1344			
gaa Glu 730	gta Val 735	gca Ala 740	ggt Gly 745
ttt Phe 750	ggt Gly 755	caa Gln 760	gtg Val 765
1392			
gaa Glu 770	gta Val 775	gca Ala 780	ggt Gly 785
ttt Phe 790	ggt Gly 795	caa Gln 800	gtg Val 805
1440			

Substitute Sequence Listing

Gly 465	Val	Asp	Tyr	Asn	Ala 470	Ser	Phe	Val	Thr	Gly 475	Gly	Ala	Phe	Ser	Leu 480	
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Asp	Gly	Val	His	Leu 485	Asn	Ser	Arg	Gly	Tyr 490	Ala	His	Thr	Ala	Asn 495	Thr	
ttt	att	cgt	gcc	atc	aat	cag	caa	tat	aag	gca	agc	att	ccg	ttg	gta	1536
Phe	Ile	Arg	Ala 500	Ile	Asn	Gln	Gln	Tyr 505	Lys	Ala	Ser	Ile	Pro 510	Leu	Val	
gat	atc	aac	gct	ttc	cca	ggc	aca	caa	tta	cct	taa					1572
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Thr	Lys	Gly 35	Glu	Ala	Asp	Phe	Ser 40	Lys	Tyr	Val	Ala	Leu 45	Gly	Asn	Ser	
Leu	Thr	Ser	Gly	Tyr	Ser	Asp 55	Gly	Ala	Leu	Tyr	Arg 60	Ser	Ala	Gln	Glu	
Asn 65	Ser	Tyr	Pro	Ala 70	Ile	Ile	Ala	Lys	Gln 75	Met	Lys	Tyr	Val	Gly 80	Gly	
Gly	Glu	Phe	Ser	Gln 85	Pro	Leu	Met	Lys	Asp 90	Asn	Ile	Gly	Gly	Phe 95	Ser	
Asp	Leu	Phe	Glu 100	Ala	Ser	Lys	His	Thr 105	Ala	Phe	Tyr	Gly	Lys 110	Leu	Glu	
Leu	Lys	Ile 115	Val	Asp	Gly	Ala	Pro 120	Thr	Pro	Val	Pro	Ser 125	Val	Pro	Lys	
Phe	Ser 130	Leu	Ala	Gln	Thr	Phe 135	Val	Lys	Gly	Asn	Phe 140	Asn	Asn	Leu	Gly	
Val 145	Pro	Gly	Ala	Lys	Ser 150	Tyr	His	Leu	Leu	Ala 155	Gln	Gly	Tyr	Gly	Asn 160	

Substitute Sequence Listing

Ile Ala Asn Leu Lys Glu Ser Lys Ala Asn Pro Tyr Phe Val Arg Phe
165 170 175

Ala Ser Gln Pro Asn Ala Ser Val Leu Ser Asp Ala Leu Ala Gln Lys
180 185 190

Pro Thr Phe Phe Thr Leu Trp Ile Gly Asn Asn Asp Val Leu Gly Tyr
195 200 205

Ala Met Asn Gly Ala Ala Ser Thr Asp Arg Lys Gly Asn Pro Asp Val
210 215 220

Thr Thr Tyr Asn Ser Asn Asp Leu Ser Asp Ala Asn Leu Val Ala Gly
225 230 235 240

Ser Ile Gln Lys Leu Val Lys Ala Leu Thr Asp Ser Gly Ala Lys Gly
245 250 255

Ala Val Ala Asn Leu Pro Tyr Val Glu Asp Ile Pro Tyr Phe Thr Thr
260 265 270

Val Pro Ala Glu Pro Leu Ser Pro Leu Asn Lys Ser Tyr Ala Thr Gln
275 280 285

Ile Glu Asn Leu Asn Lys Phe Tyr Ala Ser Leu Asn Lys Val Phe Asp
290 295 300

Ala Leu Gly Ala Ser Asp Arg Lys Ile Thr Phe Asn Ala Asp Lys Ala
305 310 315 320

Ser Gly Ala Val Ile Val Asp Lys Ser Leu Pro Asp Leu Ser Gln Lys
325 330 335

Ile Leu Ala Thr Leu Leu Lys Leu Glu Phe Pro Asn Glu Lys Ala Lys
340 345 350

Leu Leu Ala Gln Thr Phe Gly Gln Val Arg Gln Ser Lys Ala Gly Asp
355 360 365

Leu Leu Pro Leu Thr Ala Ser Arg Thr Leu Gly Lys Leu Asn Ser Glu
370 375 380

Arg Leu Ala Thr Leu Thr Lys Leu Gly Leu Pro Lys Glu Asn Ala Ala
385 390 395 400

Gln Leu Ser Met Asn Gly Leu Thr Tyr Pro Leu Gln Asp Ala Asp Val
405 410 415

Substitute Sequence Listing

Leu Thr Lys Asn Glu Val Ser Thr Ile His Glu Arg Val Asn Glu Ile
420 425 430

Asn Gln Gly Ile Gln Ala Val Ala Lys Gln Phe Asn Ile Ala Tyr Val
435 440 445

Asp Met Asn Ala Glu Met Gln Lys Leu Thr Lys Gly Phe Lys Phe Asn
450 455 460

Gly Val Asp Tyr Asn Ala Ser Phe Val Thr Gly Gly Ala Phe Ser Leu
465 470 475 480

Asp Gly Val His Leu Asn Ser Arg Gly Tyr Ala His Thr Ala Asn Thr
485 490 495

Phe Ile Arg Ala Ile Asn Gln Gln Tyr Lys Ala Ser Ile Pro Leu Val
500 505 510

Asp Ile Asn Ala Phe Pro Gly Thr Gln Leu Pro
515 520

<210> 5
<211> 1242
<212> DNA
<213> Ornithobacterium rhinotracheale

<220>
<221> CDS
<222> (1)..(1242)

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ttg aat gct tgt acc gaa gat ttt gaa ccc aca ttt tca gaa aac gca 96
Leu Asn Ala Cys Thr Glu Asp Phe Glu Pro Thr Phe Ser Glu Asn Ala
20 25 30

act cag cgt tat ata aat gtt cag aac gaa att aca gaa ttt ctt agt 144
Thr Gln Arg Tyr Ile Asn Val Gln Asn Glu Ile Thr Glu Phe Leu Ser
35 40 45

acc cct gat gct gat ttt att tta caa tac ttc cca gat gat aat cag 192
Thr Pro Asp Ala Asp Phe Ile Leu Gln Tyr Phe Pro Asp Asp Asn Gln
50 55 60

tct tat gga gga tat aat tat ttc ttg aaa ttc tca gga aaa gat aag 240
Ser Tyr Gly Gly Tyr Asn Tyr Phe Leu Lys Phe Ser Gly Lys Asp Lys
65 70 75 80

gta agt gcg gaa tca gag acc aat gaa caa gct gta agt tct act ttt 288
Val Ser Ala Glu Ser Glu Thr Asn Glu Gln Ala Val Ser Ser Thr Phe
85 90 95

Substitute Sequence Listing

cga Arg	att Ile	ctt Leu	caa Gln 100	aat Asn	gga Gly	ggt Gly	gca Ala 105	gtt Val	ctt Leu	acc Thr	ttt Phe	gat Asp	tta Leu 110	tac Tyr	aat Asn	336
gag Glu	gag Glu	cta Leu 115	cat His	gaa Glu	ttt Phe	gca Ala 120	act Thr	cct Pro	agt Ser	cca Pro	tca Ser	gaa Glu 125	tat Tyr	cgt Arg	gca Ala	384
aaa Lys	cga Arg 130	gga Gly	gat Asp	ttt Phe	gaa Glu	ttt Phe 135	ttg Leu	atc Ile	ctt Leu	aaa Lys	aaa Lys 140	agt Ser	aat Asn	gac Asp	aca Thr	432
ctt Leu 145	tat Tyr	cta Leu	aaa Lys	gga Gly	aag Lys 150	aaa Lys	aca Thr	gga Gly	aat Asn	tac Tyr 155	atg Met	aag Lys	cta Leu	tat Tyr	aaa Lys 160	480
gca Ala	ggg Gly	aat Asn	att Ile	caa Gln 165	gag Glu	att Ile	aaa Lys	agt Ser	aac Asn 170	att Ile	aga Arg	aaa Lys	gta Val	gca Ala 175	act Thr	528
aca Thr	att Ile	gat Asp	agg Arg 180	gta Val	gat Asp	ctt Leu	cca Pro	gct Ala 185	caa Gln	ggt Gly	act Thr	ata Ile	ggt Gly 190	aca Thr	gag Glu	576
cct Pro	ttg Leu	gta Val 195	ttg Leu	tca Ser	aca Thr	gga Gly	gga Gly 200	act Thr	aga Arg	aat Asn	att Ile	att Ile 205	ttt Phe	agt Ser	act Thr	624
tta Leu	aat Asn 210	ggg Gly	ggg Gly	agt Ser	ata Ile	gag Glu 215	tct Ser	aca Thr	gaa Glu	gca Ala	tcg Ser 220	tat Tyr	att Ile	ttt Phe	aca Thr	672
gaa Glu 225	aac Asn	gga Gly	att Ile	aag Lys	ttt Phe 230	tac Tyr	aaa Lys	cca Pro	gtt Val	gaa Glu 235	att Ile	aag Lys	ggg Gly	aaa Lys	gtt Val 240	720
tac Tyr	ggt Gly	gga Gly	tta Leu	att Ile 245	ttt Phe	gac Asp	gaa Glu	agt Ser	act Thr 250	caa Gln	aca Thr	tta Leu	aag Lys	tca Ser 255	gaa Glu	768
gat Asp	ggt Gly	gta Val	att Ile 260	gta Val	att Ile	aat Asn	ttg Leu	aaa Lys 265	ttt Phe	gtt Val	cct Pro	atc Ile	aac Asn 270	ttt Phe	aaa Lys	816
tca Ser	aaa Lys	gct Ala 275	tgg Trp	ttt Phe	ttg Leu	gat Asp	atg Met 280	agc Ser	aaa Lys	tca Ser	gag Glu	aat Asn 285	aca Thr	tcg Ser	gaa Glu	864
ggt Gly	tat Tyr 290	aag Lys	aaa Lys	gcc Ala	aga Arg	gca Ala 295	ggc Gly	gat Asp	agt Ser	ctt Leu	ttg Leu 300	cat His	ggt Gly	atg Met	att Ile	912
cta Leu 305	agt Ser	aaa Lys	ttt Phe	aag Lys	tta Leu 310	caa Gln	gat Asp	ttc Phe	tat Tyr	gtg Val 315	tta Leu	ggt Gly	aat Asn	ttt Phe	aga Arg 320	960
gat Asp	aat Asn	gta Val	gga Gly	ttc Phe 325	aat Asn	act Thr	ttt Phe	gtt Val	gag Glu 330	ggc Gly	tat Tyr	aac Asn	gga Gly	gca Ala 335	ttt Phe	1008
gca Ala	att Ile	tat Tyr	ggt Gly	tta Leu	agt Ser	ttc Phe	aaa Lys	gga Gly	gaa Glu	gat Asp	tca Ser	aat Asn	cca Pro	aat Asn	ctt Leu	1056

Substitute Sequence Listing

340

345

350

atc cac att gag aaa aca aaa cct gtt gaa ttt gat gct tat ttc aaa 1104
Ile His Ile Glu Lys Thr Lys Pro Val Glu Phe Asp Ala Tyr Phe Lys
355 360 365

tat gtg aat gga gtt tta gat aaa atc act aaa aat tca cct tat att 1152
Tyr Val Asn Gly Val Leu Asp Lys Ile Thr Lys Asn Ser Pro Tyr Ile
370 375 380

gta gag gag gtt cag tca gat cct aaa cgt gtg aag cta ata agt aaa 1200
Val Glu Glu Val Gln Ser Asp Pro Lys Arg Val Lys Leu Ile Ser Lys
385 390 395 400

aat gat caa gaa tta tgg ttt att ctt gat ttg ctt aaa tga 1242
Asn Asp Gln Glu Leu Trp Phe Ile Leu Asp Leu Leu Lys
405 410

<210> 6
<211> 413
<212> PRT
<213> Ornithobacterium rhinotracheale
<400> 6

Met Lys Lys Leu Ser Tyr Leu Leu Phe Ser Ile Pro Leu Leu Trp Gly
1 5 10 15

Leu Asn Ala Cys Thr Glu Asp Phe Glu Pro Thr Phe Ser Glu Asn Ala
20 25 30

Thr Gln Arg Tyr Ile Asn Val Gln Asn Glu Ile Thr Glu Phe Leu Ser
35 40 45

Thr Pro Asp Ala Asp Phe Ile Leu Gln Tyr Phe Pro Asp Asp Asn Gln
50 55 60

Ser Tyr Gly Gly Tyr Asn Tyr Phe Leu Lys Phe Ser Gly Lys Asp Lys
65 70 75 80

Val Ser Ala Glu Ser Glu Thr Asn Glu Gln Ala Val Ser Ser Thr Phe
85 90 95

Arg Ile Leu Gln Asn Gly Gly Ala Val Leu Thr Phe Asp Leu Tyr Asn
100 105 110

Glu Glu Leu His Glu Phe Ala Thr Pro Ser Pro Ser Glu Tyr Arg Ala
115 120 125

Lys Arg Gly Asp Phe Glu Phe Leu Ile Leu Lys Lys Ser Asn Asp Thr
130 135 140

Leu Tyr Leu Lys Gly Lys Lys Thr Gly Asn Tyr Met Lys Leu Tyr Lys

145	Substitute Sequence Listing										160
	155										
Ala Gly Asn Ile	Gln	Glu	Ile	Lys	Ser	Asn	Ile	Arg	Lys	Val	Ala Thr
	165					170				175	
Thr Ile Asp	Arg	Val	Asp	Leu	Pro	Ala	Gln	Gly	Thr	Ile	Gly Thr Glu
	180					185					190
Pro Leu Val	Leu	Ser	Thr	Gly	Gly	Thr	Arg	Asn	Ile	Ile	Phe Ser Thr
	195				200					205	
Leu Asn Gly	Gly	Ser	Ile	Glu	Ser	Thr	Glu	Ala	Ser	Tyr	Ile Phe Thr
	210			215					220		
Glu Asn Gly	Ile	Lys	Phe	Tyr	Lys	Pro	Val	Glu	Ile	Lys	Gly Lys Val
	225		230					235			240
Tyr Gly Gly	Leu	Ile	Phe	Asp	Glu	Ser	Thr	Gln	Thr	Leu	Lys Ser Glu
	245						250				255
Asp Gly Val	Ile	Val	Ile	Asn	Leu	Lys	Phe	Val	Pro	Ile	Asn Phe Lys
	260					265					270
Ser Lys Ala	Trp	Phe	Leu	Asp	Met	Ser	Lys	Ser	Glu	Asn	Thr Ser Glu
	275				280					285	
Gly Tyr Lys	Lys	Ala	Arg	Ala	Gly	Asp	Ser	Leu	Leu	His	Gly Met Ile
	290			295					300		
Leu Ser Lys	Phe	Lys	Leu	Gln	Asp	Phe	Tyr	Val	Leu	Gly	Asn Phe Arg
	305		310					315			320
Asp Asn Val	Gly	Phe	Asn	Thr	Phe	Val	Glu	Gly	Tyr	Asn	Gly Ala Phe
	325						330				335
Ala Ile Tyr	Gly	Leu	Ser	Phe	Lys	Gly	Glu	Asp	Ser	Asn	Pro Asn Leu
	340					345				350	
Ile His Ile	Glu	Lys	Thr	Lys	Pro	Val	Glu	Phe	Asp	Ala	Tyr Phe Lys
	355				360					365	
Tyr Val Asn	Gly	Val	Leu	Asp	Lys	Ile	Thr	Lys	Asn	Ser	Pro Tyr Ile
	370			375					380		
Val Glu Glu	Val	Gln	Ser	Asp	Pro	Lys	Arg	Val	Lys	Leu	Ile Ser Lys
	385		390					395			400

Substitute Sequence Listing

Asn Asp Gln Glu Leu Trp Phe Ile Leu Asp Leu Leu Lys
405 410

<210> 7
<211> 1023
<212> DNA
<213> Ornithobacterium rhinotracheale

<220>
<221> CDS
<222> (1)..(1023)

<400> 7	
atg aaa gat ata ttt gaa tat aca ctt cta gca tta ggt ggt ttg cta	48
Met Lys Asp Ile Phe Glu Tyr Thr Leu Leu Ala Leu Gly Gly Leu Leu	
1 5 10 15	
ctc acc aat tgc tat gat agc gat gag att gaa gta att aaa ttt gat	96
Leu Thr Asn Cys Tyr Asp Ser Asp Glu Ile Glu Val Ile Lys Phe Asp	
20 25 30	
gat tct ttt act cca gct ccg ccc acc gaa aaa aaa aga gac act ccg	144
Asp Ser Phe Thr Pro Ala Pro Pro Thr Glu Lys Lys Arg Asp Thr Pro	
35 40 45	
cta ata aat tta tta gat gat ttt gta ttc ttt aaa aaa gat gta gta	192
Leu Ile Asn Leu Leu Asp Asp Phe Val Phe Phe Lys Lys Asp Val Val	
50 55 60	
aca att ccg gta gat aaa gac aat tta gcc acc aat aat gtc atc agt	240
Thr Ile Pro Val Asp Lys Asp Asn Leu Ala Thr Asn Asn Val Ile Ser	
65 70 75 80	
ggt gaa gtc ttt aca aat aga aaa atg tct gaa aat ttt gag tat cag	288
Gly Glu Val Phe Thr Asn Arg Lys Met Ser Glu Asn Phe Glu Tyr Gln	
85 90 95	
ctt gaa tta gac caa gat tgg att agt agc aat ccg gac tta caa gcc	336
Leu Glu Leu Asp Gln Asp Trp Ile Ser Ser Asn Pro Asp Leu Gln Ala	
100 105 110	
att cca aac gga gct ttt aca atc tct gga caa aca ctc aac aaa gat	384
Ile Pro Asn Gly Ala Phe Thr Ile Ser Gly Gln Thr Leu Asn Lys Asp	
115 120 125	
gaa aga aat ggt act ttc aaa att cag ctt aat gca gag gtg gcg aaa	432
Glu Arg Asn Gly Thr Phe Lys Ile Gln Leu Asn Ala Glu Val Ala Lys	
130 135 140	
gag cta gga ggc acc tac tat ctc ccg cta aaa ttg gtt tct aaa aat	480
Glu Leu Gly Gly Thr Tyr Tyr Leu Pro Leu Lys Leu Val Ser Lys Asn	
145 150 155 160	
gat aat tta aac att tta aag gga tat gaa agt ggc gtt ttt aag cta	528
Asp Asn Leu Asn Ile Leu Lys Gly Tyr Glu Ser Gly Val Phe Lys Leu	
165 170 175	
gta ttc aaa aaa tcg tat cca atc cca gaa ggt aac aat gtt gaa gga	576
Val Phe Lys Lys Ser Tyr Pro Ile Pro Glu Gly Asn Asn Val Glu Gly	
180 185 190	

Substitute Sequence Listing

aaa Lys	aaa Lys	gga Gly 195	tat Tyr	tat Tyr	ttt Phe	gat Asp	ggt Gly 200	tta Leu	ggc Gly	aat Asn	aat Asn	ata Ile 205	cct Pro	aga Arg	aca Thr	624
gat Asp	tta Leu 210	tcg Ser	ttt Phe	aat Asn	tca Ser	aat Asn 215	tac Tyr	gcc Ala	ccc Pro	gat Asp	cat His 220	ctt Leu	ttt Phe	aaa Lys	tta Leu	672
aat Asn 225	gat Asp	gga Gly	aac Asn	caa Gln	caa Gln 230	ggg Gly	gct Ala	aat Asn	tgg Trp	tgg Trp 235	gca Ala	gac Asp	act Thr	gat Asp	gat Asp 240	720
aac Asn	aca Thr	aca Thr	tat Tyr	ctt Leu 245	gat Asp	gta Val	aaa Lys	ttc Phe	cct Pro 250	att Ile	aat Asn	aca Thr	ata Ile	aaa Lys 255	gct Ala	768
ata Ile	aaa Lys	tta Leu	tac Tyr 260	act Thr	aaa Lys	agc Ser	tat Tyr	tgg Trp 265	caa Gln	aat Asn	gct Ala	gta Val	ggc Gly 270	agt Ser	gta Val	816
aaa Lys	att Ile	gaa Glu 275	gtt Val	tct Ser	aat Asn	gat Asp	aat Asn 280	ggc Gly	aat Asn	act Thr	tgg Trp	aaa Lys 285	gaa Glu	cag Gln	gga Gly	864
att Ile	gct Ala 290	aac Asn	ttt Phe	ggg Gly	caa Gln	tat Tyr 295	tca Ser	aca Thr	gtg Val	tct Ser	act Thr 300	att Ile	gta Val	ttc Phe	act Thr	912
caa Gln 305	cca Pro	att Ile	gac Asp	att Ile	aat Asn 310	gct Ala	gtc Val	aga Arg	ata Ile	tct Ser 315	aac Asn	ttc Phe	act Thr	aga Arg	ggg Gly 320	960
gga Gly	agt Ser	agt Ser	aat Asn	ttc Phe 325	att Ile	aac Asn	att Ile	aac Asn	gag Glu 330	gtg Val	gaa Glu	gta Val	ttc Phe	aaa Lys 335	ata Ile	1008
cca Pro	agt Ser	gaa Glu	gaa Glu 340	taa												1023

<210> 8
 <211> 340
 <212> PRT
 <213> Ornithobacterium rhinotracheale

<400> 8

Met 1	Lys	Asp	Ile	Phe 5	Glu	Tyr	Thr	Leu	Leu 10	Ala	Leu	Gly	Gly	Leu 15	Leu
Leu	Thr	Asn	Cys 20	Tyr	Asp	Ser	Asp	Glu 25	Ile	Glu	Val	Ile	Lys 30	Phe	Asp
Asp	Ser	Phe 35	Thr	Pro	Ala	Pro	Pro 40	Thr	Glu	Lys	Lys	Arg 45	Asp	Thr	Pro
Leu	Ile 50	Asn	Leu	Leu	Asp	Asp 55	Phe	Val	Phe	Phe	Lys 60	Lys	Asp	Val	Val

Substitute Sequence Listing

Thr Ile Pro Val Asp Lys Asp Asn Leu Ala Thr Asn Asn Val Ile Ser
65 70 75 80

Gly Glu Val Phe Thr Asn Arg Lys Met Ser Glu Asn Phe Glu Tyr Gln
85 90 95

Leu Glu Leu Asp Gln Asp Trp Ile Ser Ser Asn Pro Asp Leu Gln Ala
100 105 110

Ile Pro Asn Gly Ala Phe Thr Ile Ser Gly Gln Thr Leu Asn Lys Asp
115 120 125

Glu Arg Asn Gly Thr Phe Lys Ile Gln Leu Asn Ala Glu Val Ala Lys
130 135 140

Glu Leu Gly Gly Thr Tyr Tyr Leu Pro Leu Lys Leu Val Ser Lys Asn
145 150 155 160

Asp Asn Leu Asn Ile Leu Lys Gly Tyr Glu Ser Gly Val Phe Lys Leu
165 170 175

Val Phe Lys Lys Ser Tyr Pro Ile Pro Glu Gly Asn Asn Val Glu Gly
180 185 190

Lys Lys Gly Tyr Tyr Phe Asp Gly Leu Gly Asn Asn Ile Pro Arg Thr
195 200 205

Asp Leu Ser Phe Asn Ser Asn Tyr Ala Pro Asp His Leu Phe Lys Leu
210 215 220

Asn Asp Gly Asn Gln Gln Gly Ala Asn Trp Trp Ala Asp Thr Asp Asp
225 230 235 240

Asn Thr Thr Tyr Leu Asp Val Lys Phe Pro Ile Asn Thr Ile Lys Ala
245 250 255

Ile Lys Leu Tyr Thr Lys Ser Tyr Trp Gln Asn Ala Val Gly Ser Val
260 265 270

Lys Ile Glu Val Ser Asn Asp Asn Gly Asn Thr Trp Lys Glu Gln Gly
275 280 285

Ile Ala Asn Phe Gly Gln Tyr Ser Thr Val Ser Thr Ile Val Phe Thr
290 295 300

Gln Pro Ile Asp Ile Asn Ala Val Arg Ile Ser Asn Phe Thr Arg Gly
305 310 315 320

Substitute Sequence Listing

Gly Ser Ser Asn Phe Ile Asn Ile Asn Glu Val Glu Val Phe Lys Ile
325 330 335

Pro Ser Glu Glu
340

<210> 9
<211> 1230
<212> DNA
<213> Ornithobacterium rhinotracheale

<220>
<221> CDS
<222> (1)..(1230)

<400> 9	
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Met Ile Lys Lys Val Phe Leu Ser Phe Val Leu Met Ala Ser Thr Gly	
1 5 10 15	
att tta tgg gca ggc gga tac cga gtt tcg ctg caa ggt gta aga caa	96
Ile Leu Trp Ala Gly Gly Tyr Arg Val Ser Leu Gln Gly Val Arg Gln	
20 25 30	
gcc gcc atg ggg gca caa ggt gta gca ctt tct cac gat gcg agt gtg	144
Ala Ala Met Gly Ala Gln Gly Val Ala Leu Ser His Asp Ala Ser Val	
35 40 45	
gca ttt ttc aac ccc gca gca ttg gct ttt gta gat gat aaa tta agt	192
Ala Phe Phe Asn Pro Ala Ala Leu Ala Phe Val Asp Asp Lys Leu Ser	
50 55 60	
att gct gtg gga ggt ttc gga att ggg att acc gca aaa tac caa aac	240
Ile Ala Val Gly Gly Phe Gly Ile Gly Ile Thr Ala Lys Tyr Gln Asn	
65 70 75 80	
cgc gaa acg ctc tat aaa gcc gaa acc gac aat ccg ctg ggg aca cca	288
Arg Glu Thr Leu Tyr Lys Ala Glu Thr Asp Asn Pro Leu Gly Thr Pro	
85 90 95	
ctt tat ctt gct aca agc tat aag cct acg gaa aaa cta gcc tta ggc	336
Leu Tyr Leu Ala Thr Ser Tyr Lys Pro Thr Glu Lys Leu Ala Leu Gly	
100 105 110	
gtg agc gta acc act ccg ttt ggg agc acc gta gac tgg gga gat aaa	384
Val Ser Val Thr Thr Pro Phe Gly Ser Thr Val Asp Trp Gly Asp Lys	
115 120 125	
tgg gct gga cgc tac atc att gat aga att gcc ctc aaa tcg ttt ttt	432
Trp Ala Gly Arg Tyr Ile Ile Asp Arg Ile Ala Leu Lys Ser Phe Phe	
130 135 140	
att cag ccc acg gca gcg tat aaa gta acc gat tgg ctc tct gtg ggg	480
Ile Gln Pro Thr Ala Tyr Lys Val Thr Asp Trp Leu Ser Val Gly	
145 150 155 160	
gct ggt gcc atc atc gct cga ggc aat gta aac att aag cgt gca ata	528
Ala Gly Ala Ile Ile Ala Arg Gly Asn Val Asn Ile Lys Arg Ala Ile	

Substitute Sequence Listing

<210> 10

<211> 409

<212> PRT

<213> Ornithobacterium rhinotracheale

<400> 10

Met Ile Lys Lys Val Phe Leu Ser Phe Val Leu Met Ala Ser Thr Gly
1 5 10 15

Ile Leu Trp Ala Gly Gly Tyr Arg Val Ser Leu Gln Gly Val Arg Gln
20 25 30

Ala Ala Met Gly Ala Gln Gly Val Ala Leu Ser His Asp Ala Ser Val
35 40 45

Ala Phe Phe Asn Pro Ala Ala Leu Ala Phe Val Asp Asp Lys Leu Ser
50 55 60

Ile Ala Val Gly Gly Phe Gly Ile Gly Ile Thr Ala Lys Tyr Gln Asn
65 70 75 80

Arg Glu Thr Leu Tyr Lys Ala Glu Thr Asp Asn Pro Leu Gly Thr Pro
85 90 95

Leu Tyr Leu Ala Thr Ser Tyr Lys Pro Thr Glu Lys Leu Ala Leu Gly
100 105 110

Val Ser Val Thr Thr Pro Phe Gly Ser Thr Val Asp Trp Gly Asp Lys
115 120 125

Trp Ala Gly Arg Tyr Ile Ile Asp Arg Ile Ala Leu Lys Ser Phe Phe
130 135 140

Ile Gln Pro Thr Ala Ala Tyr Lys Val Thr Asp Trp Leu Ser Val Gly
145 150 155 160

Ala Gly Ala Ile Ile Ala Arg Gly Asn Val Asn Ile Lys Arg Ala Ile
165 170 175

Ser Leu Gly Asn Gln Asp Ala Gly Leu Glu Ile Asp Lys Lys Gly Ala
180 185 190

His Gly Thr Gly Phe Asn Val Gly Val Tyr Ala Lys Pro Asn Asp Lys
195 200 205

Leu Asn Ile Gly Ile Ala Tyr Arg Ser Glu Val Lys Met Lys Ala Asp
210 215 220

Substitute Sequence Listing

Lys Gly Asp Ala Val Phe Lys Asn Leu Pro Ser Ile Val Lys Gly Lys
225 230 235 240

Met Pro Phe Ser Ala Lys Tyr Phe Asp Ala Gln Leu Pro Leu Pro Ala
245 250 255

Glu Leu Leu Ile Gly Ala Asn Tyr Lys Val Thr Pro Lys Leu Leu Val
260 265 270

Gly Ala Glu Ile Gly Ala Val Lys Trp Asn Ala Tyr Glu Thr Leu Asn
275 280 285

Ile Lys Leu Tyr Asn Asn Glu Glu Glu Tyr Asn Asn Thr Ser Asn Lys
290 295 300

Asn Tyr Lys Asn Thr Leu Asn Tyr Ser Ile Gly Ala Glu Tyr Leu Ile
305 310 315 320

Asn Pro Lys Ala Ala Leu Arg Leu Gly Tyr Lys Phe Asp Lys Ser Pro
325 330 335

Ser Pro Ala Asp Ser Phe Asn Pro Glu Thr Pro Thr Ile Asn Tyr His
340 345 350

Ala Phe Thr Thr Gly Phe Gly Tyr Glu Phe Glu Arg Phe Arg Val Asp
355 360 365

Ala Met Ala Glu Tyr Leu Leu Gly Asn Glu Arg Ser Phe His Asn Thr
370 375 380

Gln Tyr Asn Phe Gly Gly Asp Ile Asn Thr Gly Gly Tyr Val Phe Gly
385 390 395 400

Leu Gly Leu Ser Tyr Arg Leu Asp Lys
405

<210> 11
<211> 1140
<212> DNA
<213> Ornithobacterium rhinotracheale

<220>
<221> CDS
<222> (1)..(1140)

<400> 11
atg aag aaa ata ctt tta gca att agc ttt tcg tct ttt gtt tta agc
Met Lys Lys Ile Leu Leu Ala Ile Ser Phe Ser Ser Phe Val Leu Ser
1 5 10 15

48

Substitute Sequence Listing

tgt Cys	agc Ser	agt Ser	gat Asp 20	gat Asp	tac Tyr	act Thr	cca Pro	gcc Ala 25	aca Thr	cct Pro	aaa Lys	gaa Glu 30	aca Thr	gaa Glu	aag Lys	96
cct Pro	aag Lys	gaa Glu 35	gag Glu	gct Ala	gtg Val	gtt Val	cca Pro 40	aat Asn	aag Lys	cca Pro	gat Asp	gaa Glu 45	cca Pro	aag Lys	gct Ala	144
gat Asp	gat Asp 50	gga Gly	aac Asn	gaa Glu	aat Asn	cca Pro 55	gaa Glu	aac Asn	act Thr	gga Gly	gat Asp 60	gaa Glu	gag Glu	aat Asn	gga Gly	192
gat Asp 65	aat Asn	aca Thr	aac Asn	tcc Ser	gtt Val 70	gtc Val	ggg Gly	aag Lys	cct Pro	gat Asp 75	gat Asp	ttc Phe	cac His	atg Met	ggg Gly 80	240
aat Asn	cgc Arg	tct Ser	tat Tyr	gct Ala 85	agc Ser	tgg Trp	aaa Lys	gaa Glu	gat Asp 90	gtg Val	gat Asp	tat Tyr	atc Ile	gga Gly 95	ggt Gly	288
ttt Phe	gat Asp	att Ile	gaa Glu 100	act Thr	ctt Leu	tta Leu	agt Ser	ggg Gly 105	gct Ala	gat Asp	aat Asn	caa Gln	aaa Lys	tat Tyr	gat Asp 110	336
gcg Ala	gct Ala	tat Tyr 115	ttt Phe	agc Ser	caa Gln	ttt Phe	atc Ile 120	aag Lys	ata Ile	ttc Phe	tca Ser	tct Ser 125	agt Ser	cca Pro	aac Asn	384
gga Gly	aac Asn 130	aat Asn	ttc Phe	tac Tyr	act Thr	ttt Phe 135	cag Gln	gca Ala	gaa Glu	gac Asp	ttt Phe 140	aaa Lys	gat Asp	gtc Val	gag Glu	432
att Ile 145	aaa Lys	gac Asp	tta Leu	aag Lys	ttt Phe 150	gat Asp	att Ile	ggt Gly	aga Arg	aat Asn 155	gta Val	att Ile	aca Thr	ttt Phe	aaa Lys 160	480
act Thr	agc Ser	tac Tyr	aaa Lys	ggc Gly 165	gta Val	aaa Lys	agt Ser	gaa Glu	att Ile 170	aca Thr	tct Ser	tct Ser	tta Leu	aaa Lys 175	ttt Phe	528
gat Asp	ttg Leu	gct Ala	aat Asn 180	ttt Phe	tat Tyr	gat Asp	cga Arg	aaa Lys 185	atc Ile	aaa Lys	ata Ile	aac Asn	gaa Glu 190	gat Asp	ttc Phe	576
gtt Val	gca Ala	tct Ser 195	cac His	tac Tyr	atg Met	aga Arg	ggg Gly 200	att Ile	tat Tyr	gag Glu	gag Glu	ctt Leu 205	gga Gly	ggt Gly	ttt Phe	624
atc Ile	ggg Gly 210	aat Asn	tta Leu	tta Leu	aac Asn	tac Tyr 215	gac Asp	gat Asp	gag Glu	aaa Lys	tac Tyr 220	aat Asn	cta Leu	gag Glu	tta Leu	672
gcg Ala 225	ggg Gly	tca Ser	aaa Lys	aac Asn	aaa Lys 230	gat Asp	gaa Glu	tcc Ser	aat Asn	aac Asn 235	tct Ser	tta Leu	ggt Gly	ttt Phe	agc Ser 240	720
att Ile	cgc Arg	gta Val	aca Thr	gat Asp 245	aaa Lys	aaa Lys	gat Asp	aag Lys	tat Tyr 250	ata Ile	aca Thr	acg Thr	gtt Val	tat Tyr 255	aaa Lys	768
aac Asn	atc Ile	tca Ser	gga Gly 260	ttt Phe	agg Arg	cct Pro	ctt Leu	tct Ser 265	agt Ser	ctg Leu	cag Gln	gag Glu	gag Glu	ctt Leu	tcc Ser	816

Substitute Sequence Listing

att gct cct act tac gaa ttg cga gag aaa atc aag gag aaa ata gat Ile Ala Pro Thr Tyr Glu Leu Arg Glu Lys Ile Lys Glu Lys Ile Asp 275 280 285	864
aga aat aaa aga aac att agc cta ttg gag cta tta aaa cca tcg gta Arg Asn Lys Arg Asn Ile Ser Leu Leu Glu Leu Leu Lys Pro Ser Val 290 295 300	912
aac gaa tgg atg aag tct gcc gat ttc tac ttt aat aac act gat ttg Asn Glu Trp Met Lys Ser Ala Asp Phe Tyr Phe Asn Asn Thr Asp Leu 305 310 315 320	960
gaa tgg aga gga gat cat tat tca gct aga ggg ttt tta gat ttg tat Glu Trp Arg Gly Asp His Tyr Ser Ala Arg Gly Phe Leu Asp Leu Tyr 325 330 335	1008
ata ggt tcg cct aga ttt gag ctg att tta gca aca aaa gaa gac aat Ile Gly Ser Pro Arg Phe Glu Leu Ile Leu Ala Thr Lys Glu Asp Asn 340 345 350	1056
tgg ttg att ttg aaa gtg aaa gtg gtt cag ata aat gaa gtg cct acc Trp Leu Ile Leu Lys Val Lys Val Val Gln Ile Asn Glu Val Pro Thr 355 360 365	1104
gat ttg gtg tat agc tta aga gtt tca att aac taa Asp Leu Val Tyr Ser Leu Arg Val Ser Ile Asn 370 375	1140

<210> 12
 <211> 379
 <212> PRT
 <213> Ornithobacterium rhinotracheale

<400> 12

Met Lys Lys Ile Leu Leu Ala Ile Ser Phe Ser Ser Phe Val Leu Ser 1 5 10 15
Cys Ser Ser Asp Asp Tyr Thr Pro Ala Thr Pro Lys Glu Thr Glu Lys 20 25 30
Pro Lys Glu Glu Ala Val Val Pro Asn Lys Pro Asp Glu Pro Lys Ala 35 40 45
Asp Asp Gly Asn Glu Asn Pro Glu Asn Thr Gly Asp Glu Glu Asn Gly 50 55 60
Asp Asn Thr Asn Ser Val Val Gly Lys Pro Asp Asp Phe His Met Gly 65 70 75 80
Asn Arg Ser Tyr Ala Ser Trp Lys Glu Asp Val Asp Tyr Ile Gly Gly 85 90 95
Phe Asp Ile Glu Thr Leu Leu Ser Gly Ala Asp Asn Gln Lys Tyr Asp 100 105 110

Substitute Sequence Listing

Ala Ala Tyr Phe Ser Gln Phe Ile Lys Ile Phe Ser Ser Ser Pro Asn
115 120 125

Gly Asn Asn Phe Tyr Thr Phe Gln Ala Glu Asp Phe Lys Asp Val Glu
130 135 140

Ile Lys Asp Leu Lys Phe Asp Ile Gly Arg Asn Val Ile Thr Phe Lys
145 150 155 160

Thr Ser Tyr Lys Gly Val Lys Ser Glu Ile Thr Ser Ser Leu Lys Phe
165 170 175

Asp Leu Ala Asn Phe Tyr Asp Arg Lys Ile Lys Ile Asn Glu Asp Phe
180 185 190

Val Ala Ser His Tyr Met Arg Gly Ile Tyr Glu Glu Leu Gly Gly Phe
195 200 205

Ile Gly Asn Leu Leu Asn Tyr Asp Asp Glu Lys Tyr Asn Leu Glu Leu
210 215 220

Ala Gly Ser Lys Asn Lys Asp Glu Ser Asn Asn Ser Leu Gly Phe Ser
225 230 235 240

Ile Arg Val Thr Asp Lys Lys Asp Lys Tyr Ile Thr Thr Val Tyr Lys
245 250 255

Asn Ile Ser Gly Phe Arg Pro Leu Ser Ser Leu Gln Glu Glu Leu Ser
260 265 270

Ile Ala Pro Thr Tyr Glu Leu Arg Glu Lys Ile Lys Glu Lys Ile Asp
275 280 285

Arg Asn Lys Arg Asn Ile Ser Leu Leu Glu Leu Leu Lys Pro Ser Val
290 295 300

Asn Glu Trp Met Lys Ser Ala Asp Phe Tyr Phe Asn Asn Thr Asp Leu
305 310 315 320

Glu Trp Arg Gly Asp His Tyr Ser Ala Arg Gly Phe Leu Asp Leu Tyr
325 330 335

Ile Gly Ser Pro Arg Phe Glu Leu Ile Leu Ala Thr Lys Glu Asp Asn
340 345 350

Trp Leu Ile Leu Lys Val Lys Val Val Gln Ile Asn Glu Val Pro Thr

355

Substitute Sequence Listing

360

365

Asp Leu Val Tyr Ser Leu Arg Val Ser Ile Asn
 370 375

<210> 13
 <211> 918
 <212> DNA
 <213> Ornithobacterium rhinotracheale

<220>
 <221> CDS
 <222> (1)..(918)

<400> 13
 atg att gta aaa gac ttt tca gac tat aca ttc cga tgt tct caa tta 48
 Met Ile Val Lys Asp Phe Ser Asp Tyr Thr Phe Arg Cys Ser Gln Leu
 1 5 10 15
 ggt aag tta atg gtt ggt gtc aag cca cca tta acc cct aat caa gag 96
 Gly Lys Leu Met Val Gly Val Lys Pro Pro Leu Thr Pro Asn Gln Glu
 20 25 30
 aag ttg ctc aca gac tta gag ggc aaa atg gaa gct ggg acc att acc 144
 Lys Leu Leu Thr Asp Leu Glu Gly Lys Met Glu Ala Gly Thr Ile Thr
 35 40 45
 aaa aag caa atc atc act tat ggt gaa ttg ctt tcc aag aaa aac caa 192
 Lys Lys Gln Ile Ile Thr Tyr Gly Glu Leu Leu Ser Lys Lys Asn Gln
 50 55 60
 aag ctt gaa tta tct gca agt gta aag tct tac tta gcc gac att cat 240
 Lys Leu Glu Leu Ser Ala Ser Val Lys Ser Tyr Leu Ala Asp Ile His
 65 70 75 80
 aaa gaa gtc ttt ttt ggt cgt gat aag gaa ttg acc aat aaa tat cta 288
 Lys Glu Val Phe Phe Gly Arg Asp Lys Glu Leu Thr Asn Lys Tyr Leu
 85 90 95
 tca aaa ggc att caa gta gaa gaa aag agc ata acg ctc tat tcc gat 336
 Ser Lys Gly Ile Gln Val Glu Glu Lys Ser Ile Thr Leu Tyr Ser Asp
 100 105 110
 gtc tgt aac aag tta ttc cta aag aat aaa aag ttt tac aaa aac gat 384
 Val Cys Asn Lys Leu Phe Leu Lys Asn Lys Lys Phe Tyr Lys Asn Asp
 115 120 125
 ttt att caa ggt acg cca gat aac acg caa gac aaa atc aga gat atc 432
 Phe Ile Gln Gly Thr Pro Asp Asn Thr Gln Asp Lys Ile Arg Asp Ile
 130 135 140
 aaa agt agt tgg gac ttc tca acc ttt cct cta cac gcc gat gaa acg 480
 Lys Ser Ser Trp Asp Phe Ser Thr Phe Pro Leu His Ala Asp Glu Thr
 145 150 155 160
 cca acc aaa gac tat gaa tgg cag ttg caa ggt tat atg gaa tta aca 528
 Pro Thr Lys Asp Tyr Glu Trp Gln Leu Gln Gly Tyr Met Glu Leu Thr
 165 170 175
 ggc tta aaa gaa gct gag ttg att tat tgc ttg gtt gat acg cct cat 576

Substitute Sequence Listing

Gly	Leu	Lys	Glu	Ala	Glu	Leu	Ile	Tyr	Cys	Leu	Val	Asp	Thr	Pro	His	
			180					185					190			
aaa	att	gta	gaa	gat	gaa	atc	cga	aga	atg	gac	tgg	aag	cat	aat	tta	624
Lys	Ile	Val	Glu	Asp	Glu	Ile	Arg	Arg	Met	Asp	Trp	Lys	His	Asn	Leu	
		195					200					205				
ctt	gac	att	aac	ggc	gaa	gtg	aga	gcc	gag	aca	aga	gat	tta	gta	gtt	672
Leu	Asp	Ile	Asn	Gly	Glu	Val	Arg	Ala	Glu	Thr	Arg	Asp	Leu	Val	Val	
	210					215					220					
gag	att	gtg	tct	aac	tta	att	tat	acc	aag	caa	ggc	ttg	gaa	gac	ttt	720
Glu	Ile	Val	Ser	Asn	Leu	Ile	Tyr	Thr	Lys	Gln	Gly	Leu	Glu	Asp	Phe	
225					230					235					240	
tgt	cag	cag	tcc	gca	gtc	ata	aac	aaa	gat	tgg	ttc	acg	gac	ttt	gag	768
Cys	Gln	Gln	Ser	Ala	Val	Ile	Asn	Lys	Asp	Trp	Phe	Thr	Asp	Phe	Glu	
				245					250					255		
gaa	ata	cca	caa	gaa	ttg	aga	att	aaa	gtt	ttt	cac	ttt	gag	cat	caa	816
Glu	Ile	Pro	Gln	Glu	Leu	Arg	Ile	Lys	Val	Phe	His	Phe	Glu	His	Gln	
			260					265					270			
aaa	gag	atg	att	agc	gca	ctc	tac	gag	caa	ata	gga	aga	tgt	aga	gcg	864
Lys	Glu	Met	Ile	Ser	Ala	Leu	Tyr	Glu	Gln	Ile	Gly	Arg	Cys	Arg	Ala	
		275					280					285				
cat	tta	aac	gac	ttg	acc	atg	aaa	atg	gca	aca	cga	tta	gaa	tta	ata	912
His	Leu	Asn	Asp	Leu	Thr	Met	Lys	Met	Ala	Thr	Arg	Leu	Glu	Leu	Ile	
	290					295					300					
gca	taa															918
Ala																
305																

<210> 14
 <211> 305
 <212> PRT
 <213> Ornithobacterium rhinotracheale
 <400> 14

Met	Ile	Val	Lys	Asp	Phe	Ser	Asp	Tyr	Thr	Phe	Arg	Cys	Ser	Gln	Leu
1				5					10					15	
Gly	Lys	Leu	Met	Val	Gly	Val	Lys	Pro	Pro	Leu	Thr	Pro	Asn	Gln	Glu
			20					25					30		
Lys	Leu	Leu	Thr	Asp	Leu	Glu	Gly	Lys	Met	Glu	Ala	Gly	Thr	Ile	Thr
		35					40					45			
Lys	Lys	Gln	Ile	Ile	Thr	Tyr	Gly	Glu	Leu	Leu	Ser	Lys	Lys	Asn	Gln
	50					55					60				
Lys	Leu	Glu	Leu	Ser	Ala	Ser	Val	Lys	Ser	Tyr	Leu	Ala	Asp	Ile	His
65					70					75					80

Substitute Sequence Listing

Lys Glu Val Phe Phe Gly Arg Asp Lys Glu Leu Thr Asn Lys Tyr Leu
85 90 95

Ser Lys Gly Ile Gln Val Glu Glu Lys Ser Ile Thr Leu Tyr Ser Asp
100 105 110

Val Cys Asn Lys Leu Phe Leu Lys Asn Lys Lys Phe Tyr Lys Asn Asp
115 120 125

Phe Ile Gln Gly Thr Pro Asp Asn Thr Gln Asp Lys Ile Arg Asp Ile
130 135 140

Lys Ser Ser Trp Asp Phe Ser Thr Phe Pro Leu His Ala Asp Glu Thr
145 150 155 160

Pro Thr Lys Asp Tyr Glu Trp Gln Leu Gln Gly Tyr Met Glu Leu Thr
165 170 175

Gly Leu Lys Glu Ala Glu Leu Ile Tyr Cys Leu Val Asp Thr Pro His
180 185 190

Lys Ile Val Glu Asp Glu Ile Arg Arg Met Asp Trp Lys His Asn Leu
195 200 205

Leu Asp Ile Asn Gly Glu Val Arg Ala Glu Thr Arg Asp Leu Val Val
210 215 220

Glu Ile Val Ser Asn Leu Ile Tyr Thr Lys Gln Gly Leu Glu Asp Phe
225 230 235 240

Cys Gln Gln Ser Ala Val Ile Asn Lys Asp Trp Phe Thr Asp Phe Glu
245 250 255

Glu Ile Pro Gln Glu Leu Arg Ile Lys Val Phe His Phe Glu His Gln
260 265 270

Lys Glu Met Ile Ser Ala Leu Tyr Glu Gln Ile Gly Arg Cys Arg Ala
275 280 285

His Leu Asn Asp Leu Thr Met Lys Met Ala Thr Arg Leu Glu Leu Ile
290 295 300

Ala
305

<210> 15
<211> 888
<212> DNA

Substitute Sequence Listing

<213> Ornithobacterium rhinotracheale

<220>

<221> CDS

<222> (1)..(888)

<400> 15

atg aac gaa tta gcg aaa aac gac atc aag tca ttg tta aaa agt gcc	48
Met Asn Glu Leu Ala Lys Asn Asp Ile Lys Ser Leu Leu Lys Ser Ala	
1 5 10 15	

gac atc aac aaa aga ttt gag caa ttg ctc ggc aaa aaa gca caa ggc	96
Asp Ile Asn Lys Arg Phe Glu Gln Leu Leu Gly Lys Lys Ala Gln Gly	
20 25 30	

ttt atc tca tca gtc ttg cag acg gca caa aat aac aga ttg tta gcg	144
Phe Ile Ser Ser Val Leu Gln Thr Ala Gln Asn Asn Arg Leu Leu Ala	
35 40 45	

aca gcc gac cca aag acc att cta aac gct gca gta aca gcc gcg act	192
Thr Ala Asp Pro Lys Thr Ile Leu Asn Ala Ala Val Thr Ala Ala Thr	
50 55 60	

tta gat ttg cca att aat cag aat tta ggt tac gcc tac atc gtg cct	240
Leu Asp Leu Pro Ile Asn Gln Asn Leu Gly Tyr Ala Tyr Ile Val Pro	
65 70 75 80	

tac aaa ggg cag gcg caa ttc caa tta ggc tgg aag ggc ttt gta gca	288
Tyr Lys Gly Gln Ala Gln Phe Gln Leu Gly Trp Lys Gly Phe Val Ala	
85 90 95	

tta gct aaa aga agt ggc gca tat ttg aaa atg aat gta gta act gtc	336
Leu Ala Lys Arg Ser Gly Ala Tyr Leu Lys Met Asn Val Val Thr Val	
100 105 110	

tat caa aat caa ttc aaa tcc tac aat cgc tta aca gaa gaa tta gat	384
Tyr Gln Asn Gln Phe Lys Ser Tyr Asn Arg Leu Thr Glu Glu Leu Asp	
115 120 125	

gcc gat ttc aca atc gaa ggc aat ggt gaa gta gtt ggt tat gca gcc	432
Ala Asp Phe Thr Ile Glu Gly Asn Gly Glu Val Val Gly Tyr Ala Ala	
130 135 140	

tat ttc aaa gaa atc aat ggt ttt gaa aag ctt tcg ttt tgg tca att	480
Tyr Phe Lys Glu Ile Asn Gly Phe Glu Lys Leu Ser Phe Trp Ser Ile	
145 150 155 160	

gag caa gta aaa aaa cac gcc acc aaa tac tct caa act tat ggt aaa	528
Glu Gln Val Lys Lys His Ala Thr Lys Tyr Ser Gln Thr Tyr Gly Lys	
165 170 175	

aaa tca cgc tcg ggg gca tta atg ttt tcg cct tgg aat gat gaa gac	576
Lys Ser Arg Ser Gly Ala Leu Met Phe Ser Pro Trp Asn Asp Glu Asp	
180 185 190	

cag ttt gac gca atg gct atg aag act gtc tta aaa aac acg ctc tca	624
Gln Phe Asp Ala Met Ala Met Lys Thr Val Leu Lys Asn Thr Leu Ser	
195 200 205	

aag ttt ggg aca ctc tca att gaa atg caa atg gcg caa atg gca gac	672
Lys Phe Gly Thr Leu Ser Ile Glu Met Gln Met Ala Gln Met Ala Asp	
210 215 220	

Substitute Sequence Listing

caa gca gtc atc aag aac gag ggg gag tac gag tat ata gac aat acc Gln Ala Val Ile Lys Asn Glu Gly Glu Tyr Glu Tyr Ile Asp Asn Thr 225 230 235 240	720
ata gac att gaa gct gaa agt gcc gaa gaa gaa gcc aat cgt att atg Ile Asp Ile Glu Ala Glu Ser Ala Glu Glu Glu Ala Asn Arg Ile Met 245 250 255	768
aaa ttt att gat aaa gcc gaa agc att gaa gcc tta gag gaa tta aaa Lys Phe Ile Asp Lys Ala Glu Ser Ile Glu Ala Leu Glu Glu Leu Lys 260 265 270	816
tca tca gtt gat gag aat ggc gat tta gag tta tta gcc tat tac gac Ser Ser Val Asp Glu Asn Gly Asp Leu Glu Leu Leu Ala Tyr Tyr Asp 275 280 285	864
aac aga aaa aat gaa tta aaa tga Asn Arg Lys Asn Glu Leu Lys 290 295	888

<210> 16
<211> 295
<212> PRT
<213> Ornithobacterium rhinotracheale

<400> 16

Met Asn Glu Leu Ala Lys Asn Asp Ile Lys Ser Leu Leu Lys Ser Ala
1 5 10 15

Asp Ile Asn Lys Arg Phe Glu Gln Leu Leu Gly Lys Lys Ala Gln Gly
20 25 30

Phe Ile Ser Ser Val Leu Gln Thr Ala Gln Asn Asn Arg Leu Leu Ala
35 40 45

Thr Ala Asp Pro Lys Thr Ile Leu Asn Ala Ala Val Thr Ala Ala Thr
50 55 60

Leu Asp Leu Pro Ile Asn Gln Asn Leu Gly Tyr Ala Tyr Ile Val Pro
65 70 75 80

Tyr Lys Gly Gln Ala Gln Phe Gln Leu Gly Trp Lys Gly Phe Val Ala
85 90 95

Leu Ala Lys Arg Ser Gly Ala Tyr Leu Lys Met Asn Val Val Thr Val
100 105 110

Tyr Gln Asn Gln Phe Lys Ser Tyr Asn Arg Leu Thr Glu Glu Leu Asp
115 120 125

Ala Asp Phe Thr Ile Glu Gly Asn Gly Glu Val Val Gly Tyr Ala Ala
130 135 140

Substitute Sequence Listing

Tyr Phe Lys Glu Ile Asn Gly Phe Glu Lys Leu Ser Phe Trp Ser Ile
145 150 155 160

Glu Gln Val Lys Lys His Ala Thr Lys Tyr Ser Gln Thr Tyr Gly Lys
165 170 175

Lys Ser Arg Ser Gly Ala Leu Met Phe Ser Pro Trp Asn Asp Glu Asp
180 185 190

Gln Phe Asp Ala Met Ala Met Lys Thr Val Leu Lys Asn Thr Leu Ser
195 200 205

Lys Phe Gly Thr Leu Ser Ile Glu Met Gln Met Ala Gln Met Ala Asp
210 215 220

Gln Ala Val Ile Lys Asn Glu Gly Glu Tyr Glu Tyr Ile Asp Asn Thr
225 230 235 240

Ile Asp Ile Glu Ala Glu Ser Ala Glu Glu Glu Ala Asn Arg Ile Met
245 250 255

Lys Phe Ile Asp Lys Ala Glu Ser Ile Glu Ala Leu Glu Glu Leu Lys
260 265 270

Ser Ser Val Asp Glu Asn Gly Asp Leu Glu Leu Leu Ala Tyr Tyr Asp
275 280 285

Asn Arg Lys Asn Glu Leu Lys
290 295